

Amendment to the Claims:

Please amend the claims as follows:

Please cancel claims 14 to 15, without prejudice.

This listing of claims will replace all prior versions, and listing, of claims in the application:

Listing of Claims:

Claim 1 (currently amended): A recombinant expression system comprising a host cell comprising a nucleic acid encoding a phytase enzyme (i) having the amino acid sequence as set forth in SEQ ID NO:2, or (ii) having an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, wherein the nucleic acid is operably linked to a transcription control sequence.

Claim 2 (currently amended): A vector comprising a nucleic acid (i) comprising a sequence as set forth in SEQ ID NO:1, (ii) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2, or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, or, (iii) encoding a phytase comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, [[with]] wherein the phytase sequence has at least one conservative amino acid substitution [[substitutions]], wherein the conservative amino acid substitutions comprise replacements substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, [[or,]] (b) an interchange of the hydroxyl residues Ser and Thr, [[or,]] (c) an exchange of the acidic residues Asp and Glu, [[or,]] (d) a substitution between the amide residues Asn and Gln, [[or,]] (e) an exchange of the basic residues Lys and Arg, [[or,]] (f) a replacement [[replacements]] among the aromatic residues Phe, Tyr, [[or]] (g) any combination of a, b, c, d, e or f [[thereof]], or (iv) encoding a phytase comprising an enzymatically active fragment of (i), (ii) or (iii) fragments thereof.

Claim 3 (currently amended): The expression system of claim 1 wherein the transcription control sequence comprises a constitutive promoter.

Claim 4 (currently amended): The expression system of claim 1 wherein the transcription control sequence comprises a tissue-specific promoter.

Claim 5 (previously presented): The expression system of claim 1 wherein said host cell is a prokaryotic cell.

Claim 6 (previously presented): The expression system of claim 1 wherein said host cell is a eukaryotic cell.

Claim 7 (previously presented): The expression system of claim 1 wherein said host cell is a plant cell.

Claim 8 (previously presented): The expression system of claim 1 wherein the nucleic acid further comprises a sequence encoding a signal peptide or a transit peptide.

Claim 9 (previously presented): The expression system of claim 8 wherein said signal peptide is a pathogenesis-related (PR) protein PR-S signal peptide from tobacco.

Claim 10 (currently amended): A prokaryotic cell comprising an exogenous nucleic acid encoding a phytase enzyme, wherein the nucleic acid is operably linked to a transcriptional control sequence and the phytase enzyme (i) is encoded by a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, (ii) comprises an amino acid sequence as set forth in SEQ ID NO:2, or comprises an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, or, (iii) comprises ~~[[a]]~~ an amino acid sequence as set forth in SEQ ID NO:2 or an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, ~~[[with]]~~ having at least one conservative amino acid substitution ~~[[substitutions]]~~, wherein ~~the conservative amino acid substitutions comprise replacements~~ substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, ~~[[or,]]~~ (b) an interchange of the hydroxyl residues Ser and Thr, ~~[[or,]]~~ (c) an exchange of the acidic residues Asp and Glu, ~~[[or,]]~~ (d) a substitution between the amide residues Asn and Gln, ~~[[or,]]~~ (e) an

exchange of the basic residues Lys and Arg, [[or,]] (f) a replacement [[replacements]] among the aromatic residues Phe, Tyr, or (g) any combination of a, b, c, d, e or f [[thereof]], or (iv) encoding a phytase comprising an enzymatically active fragment of (i), (ii) or (iii) fragments thereof.

Claim 11 (currently amended): A eukaryotic cell comprising an exogenous nucleic acid encoding a phytase enzyme, wherein the nucleic acid is operably linked to a transcriptional control sequence and the phytase enzyme (i) is encoded by a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, (ii) comprises an amino acid sequence as set forth in SEQ ID NO:2, or comprises an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, or, (iii) comprises [[a]] an amino acid sequence as set forth in SEQ ID NO:2 or comprises an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, [[with]] having at least one conservative amino acid substitution [[substitutions]], wherein the conservative amino acid substitutions comprise replacements substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, [[or,]] (b) an interchange of the hydroxyl residues Ser and Thr, [[or,]] (c) an exchange of the acidic residues Asp and Glu, [[or,]] (d) a substitution between the amide residues Asn and Gln, [[or,]] (e) an exchange of the basic residues Lys and Arg, [[or,]] (f) a replacement [[replacements]] among the aromatic residues Phe, Tyr, or (g) any combination of a, b, c, d, e or f [[thereof]], or (iv) encoding a phytase comprising an enzymatically active fragment of (i), (ii) or (iii) fragments thereof.

Claim 12 (currently amended): A cell comprising an exogenous nucleic acid encoding a phytase enzyme, wherein the nucleic acid is operably linked to a transcriptional control sequence and the phytase enzyme (i) is encoded by a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, (ii) comprises an amino acid sequence as set forth in SEQ ID NO:2 or comprises an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, or, (iii) comprises [[a]] an amino acid sequence as set forth in SEQ ID NO:2 or comprises an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, [[with]]

having at least one conservative amino acid substitution [[substitutions]], wherein the conservative amino acid ~~substitutions comprise replacements~~ substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, [[or,]] (b) an interchange of the hydroxyl residues Ser and Thr, [[or,]] (c) an exchange of the acidic residues Asp and Glu, [[or,]] (d) a substitution between the amide residues Asn and Gln, [[or,]] (e) an exchange of the basic residues Lys and Arg, [[or,]] (f) a replacement [[replacements]] among the aromatic residues Phe, Tyr, or (g) any combination of a, b, c, d, e or f [[thereof]], or (iv) encoding a phytase comprising an enzymatically active fragment of (i), (ii) or (iii) fragments thereof.

Claim 13 (previously presented): A method for making a phytase in a cell comprising:

(a) culturing the cell of claim 12 under conditions wherein the exogenous nucleic acid encoding the phytase enzyme is expressed.

Claims 14 to 15 (canceled)

Claim 16 (currently amended): An expression system for making a polypeptide having phytase activity comprising a host cell and an exogenous nucleic acid, wherein the host cell is capable of expressing the exogenous nucleic acid, and the exogenous nucleic acid encodes the polypeptide having phytase activity, and the polypeptide having phytase activity (i) is encoded by a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, (ii) comprises an amino acid sequence as set forth in SEQ ID NO:2, or comprises an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, or, (iii) comprises [[a]] an amino acid sequence as set forth in SEQ ID NO:2 or comprises an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, [[with]] having at least one conservative amino acid substitution [[substitutions]], wherein the conservative amino acid ~~substitutions comprise replacements~~ substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, [[or,]] (b) an interchange of the hydroxyl residues Ser and Thr, [[or,]] (c) an exchange of the acidic residues Asp and Glu, [[or,]] (d) a substitution between

the amide residues Asn and Gln, ~~[[or,]]~~ (e) an exchange of the basic residues Lys and Arg, ~~[[or,]]~~ (f) a replacement ~~[[replacements]]~~ among the aromatic residues Phe, Tyr, or (g) any combination of a, b, c, d, e or f ~~[[thereof]]~~, or (iv) encoding a phytase comprising an enzymatically active fragment of (i), (ii) or (iii) fragments thereof.

Claim 17 (previously presented): The expression system of claim 16, wherein the exogenous nucleic acid is operably linked to a transcriptional control sequence.

Claim 18 (previously presented): The expression system of claim 7 wherein said plant cell is a higher plant cell.

Claim 19 (previously presented): The expression system of claim 8 wherein the signal peptide is a secretory signal peptide.

Claim 20 (previously presented): The expression system of claim 1 or claim 16, wherein the nucleic acid further comprises a promoter sequence, a secretory sequence, a stabilizing sequence, a targeting sequence or a termination sequence.

Claim 21 (currently amended): The expression system of claim 1 or claim 16, wherein the nucleic acid further comprises a vector sequence.

Claim 22 (previously presented): The expression system ~~[[method]]~~ of claim 21, wherein the vector comprises a cloning vector, an expression vector, a bacterial vector, a plasmid, a viral particle, a phage, chromosomal DNA sequences, nonchromosomal DNA sequences, synthetic DNA sequences, a vaccinia vector, an adenovirus vector, a fowl pox virus, a pseudorabies vector or a combination thereof.

Claim 23 (previously presented): The vector of claim 2, wherein the vector comprises a cloning vector, an expression vector, a bacterial vector, a plasmid, a viral particle, a phage, chromosomal DNA sequences, nonchromosomal DNA sequences, synthetic DNA

sequences, a vaccinia vector, an adenovirus vector, a fowl pox virus, a pseudorabies vector or a combination thereof.

Claim 24 (currently amended): The eukaryotic cell [[method]] of claim 11, wherein the eukaryotic cell is a plant cell.

Claim 25 (currently amended): The eukaryotic cell [[method]] of claim 24, wherein the plant cell is a higher plant cell.

Claim 26 (currently amended): The eukaryotic cell [[method]] of claim 24, wherein the plant cell [[comprises]] is a seed cell.

Claim 27 (currently amended): The eukaryotic cell [[method]] of claim 24, wherein the plant cell [[comprises]] is an edible flower cell, a cauliflower cell, an artichoke cell, a fruit cell, an apple cell, a banana cell, a berry cell, a currant cell, a cherry cell, a cucumber cell, a grape cell, a lemon cell, a melon cell, a nut cell, an orange cell, a peach cell, a pear cell, a plum cell, a strawberry cell, a tomato cell, a leaf cell, an alfalfa cell, a cabbage cell, an endive cell, a leek cell, a lettuce cell, a spinach cell, a tobacco cell, a root cell, an arrowroot cell, a beet cell, a carrot cell, a cassava cell, a turnip cell, a radish cell, a yam cell, a sweet potato cell, a bean cell, a pea cell, a soybean cell, a wheat cell, a barley cell, a corn cell, a rice cell, a rapeseed cell, a millet cell, a sunflower cell, an oat cell, a tuber cell, a kohlrabi cell or a potato cell.

Claim 28 (previously presented): The method of claim 13, further comprising converting the cell into a composition suitable for animal feed.

Claim 29 (previously presented): The method of claim 13, wherein the cell is a prokaryotic cell or a eukaryotic cell.

Claim 30 (previously presented): The method of claim 29, wherein the eukaryotic cell is a plant cell.

Claim 31 (previously presented): The method of claim 30, wherein the plant cell is a higher plant cell.

Claim 32 (currently amended): The method of claim 30, wherein the plant cell [[comprises]] is a seed cell.

Claim 33 (currently amended): The method of claim 30 wherein the plant cell [[comprises]] is an edible flower cell, a cauliflower cell, an artichoke cell, a fruit cell, an apple cell, a banana cell, a berry cell, a currant cell, a cherry cell, a cucumber cell, a grape cell, a lemon cell, a melon cell, a nut cell, an orange cell, a peach cell, a pear cell, a plum cell, a strawberry cell, a tomato cell, a leaf cell, an alfalfa cell, a cabbage cell, an endive cell, a leek cell, a lettuce cell, a spinach cell, a tobacco cell, a root cell, an arrowroot cell, a beet cell, a carrot cell, a cassava cell, a turnip cell, a radish cell, a yam cell, a sweet potato cell, a bean cell, a pea cell, a soybean cell, a wheat cell, a barley cell, a corn cell, a rice cell, a rapeseed cell, a millet cell, a sunflower cell, an oat cell, a tuber cell, a kohlrabi cell or a potato cell.

Claim 34 (previously presented): The expression system of claim 16, wherein the phytase activity comprises hydrolyzing inorganic phosphate from phytate.

Claim 35 (new): A vector comprising a nucleic acid (i) comprising a sequence as set forth in SEQ ID NO:1; (ii) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432; (iii) encoding a phytase comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, wherein the phytase has at least one conservative amino acid substitution, wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys

and Arg, or (f) a replacement among the aromatic residues Phe, Tyr; or, (iii) comprising a sequence that is the complement of a sequence of (i), (ii) or (iii).

Claim 36 (new): A cell comprising a vector comprising a nucleic acid (i) comprising a sequence as set forth in SEQ ID NO:1; (ii) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432; (iii) encoding a phytase comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, wherein the phytase has at least one conservative amino acid substitution, wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, or (f) a replacement among the aromatic residues Phe, Tyr; or, (iii) comprising a sequence that is the complement of a sequence of (i), (ii) or (iii).

Claim 37 (new): An expression system comprising a nucleic acid (i) comprising a sequence as set forth in SEQ ID NO:1; (ii) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432; (iii) encoding a phytase comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, wherein the phytase has at least one conservative amino acid substitution, wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, or (f) a replacement among the aromatic residues Phe, Tyr; or, (iii) comprising a sequence that is the complement of a sequence of (i), (ii) or (iii).



Claim 38 (new): A cloning vector comprising a nucleic acid (i) comprising a sequence as set forth in SEQ ID NO:1; (ii) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432; (iii) encoding a phytase comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, wherein the phytase has at least one conservative amino acid substitution, wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, or (f) a replacement among the aromatic residues Phe, Tyr; or, (iii) comprising a sequence that is the complement of a sequence of (i), (ii) or (iii).

Claim 39 (new): An expression vector comprising a nucleic acid (i) comprising a sequence as set forth in SEQ ID NO:1; (ii) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432; (iii) encoding a phytase comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, wherein the phytase has at least one conservative amino acid substitution, wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, or (f) a replacement among the aromatic residues Phe, Tyr; or, (iii) comprising a sequence that is the complement of a sequence of (i), (ii) or (iii).

Claim 40 (new): A bacterial vector comprising a nucleic acid (i) comprising a sequence as set forth in SEQ ID NO:1; (ii) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432; (iii) encoding a phytase comprising an amino acid

sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, wherein the phytase has at least one conservative amino acid substitution, wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, or (f) a replacement among the aromatic residues Phe, Tyr; or, (iii) comprising a sequence that is the complement of a sequence of (i), (ii) or (iii).

Claim 41 (new): A plasmid comprising a nucleic acid (i) comprising a sequence as set forth in SEQ ID NO:1; (ii) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432; (iii) encoding a phytase comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, wherein the phytase has at least one conservative amino acid substitution, wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, or (f) a replacement among the aromatic residues Phe, Tyr; or, (iii) comprising a sequence that is the complement of a sequence of (i), (ii) or (iii).

Claim 42 (new): A viral particle comprising a nucleic acid (i) comprising a sequence as set forth in SEQ ID NO:1; (ii) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432; (iii) encoding a phytase comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, wherein the phytase has at least one conservative amino acid substitution, wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an

interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, or (f) a replacement among the aromatic residues Phe, Tyr; or, (iii) comprising a sequence that is the complement of a sequence of (i), (ii) or (iii).

Claim 43 (new): A phage comprising a nucleic acid (i) comprising a sequence as set forth in SEQ ID NO:1; (ii) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432; (iii) encoding a phytase comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, wherein the phytase has at least one conservative amino acid substitution, wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, or (f) a replacement among the aromatic residues Phe, Tyr; or, (iii) comprising a sequence that is the complement of a sequence of (i), (ii) or (iii).

Claim 44 (new): A phage comprising a nucleic acid (i) comprising a sequence as set forth in SEQ ID NO:1; (ii) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432; (iii) encoding a phytase comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, wherein the phytase has at least one conservative amino acid substitution, wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, or (f) a replacement among the aromatic residues Phe, Tyr; or, (iii) comprising a sequence that is the complement of a sequence of (i), (ii) or (iii).

Claim 45 (new): A recombinant expression system comprising a nucleic acid encoding a phytase enzyme (i) having the amino acid sequence as set forth in SEQ ID NO:2, or (ii) having an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432.

Claim 46 (new): A method for making a phytase in a cell comprising culturing the cell under conditions wherein an exogenous nucleic acid encoding the phytase is expressed, wherein the exogenous nucleic acid comprises a nucleic acid (i) comprising a sequence as set forth in SEQ ID NO:1; (ii) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432; (iii) encoding a phytase comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, wherein the phytase has at least one conservative amino acid substitution, wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, or (f) a replacement among the aromatic residues Phe, Tyr; or, (iii) comprising a sequence that is the complement of a sequence of (i), (ii) or (iii).